

Want To Know What a Gene Does?

Use a Little MAGIC

Do you believe in MAGIC? Agricultural Research Service plant geneticist Peter Balint-Kurti and colleagues at Purdue University do, especially when it comes to testing gene function in maize plants. But these scientists aren't using card tricks or pulling rabbits out of hats. For them, MAGIC is an acronym that stands for "mutant-assisted gene identification and characterization."

"MAGIC is a gene-centered approach that uses mutant genes or other genetic variants controlling a trait of interest as 'reporters' to identify novel genes and variants for that trait," explains Balint-Kurti, who is in the ARS Plant Science Research Unit in Raleigh, North Carolina. He teamed up with Guri Johal and Cliff Weil at Purdue to create MAGIC.

MAGIC offers researchers a new way of sifting through the large amount of natural genetic variation present in most plant species to identify and map versions of genes important for the control of specific agriculturally useful traits. MAGIC starts out with a clearly defined mutation affecting a trait of interest and then identifies other genomic regions that affect the same trait. By using a mutation, the trait in question can be exaggerated, making it easier to spot other genes affecting the trait that would not otherwise be readily detectable. The process involves crossing the mutant gene into plants with different genetic backgrounds and then evaluating the offspring for the strength of the mutant phenotype.

PETER BALINT-KURTI (D1933-1)



Two leaves from sibling plants. The plant on the left has the *Rp1-D21* gene, which causes hypersensitive response (the mottled yellow appearance). The plant on the right doesn't have this gene.



JOE BUNDY (D1934-1)

ARS plant geneticist Peter Balint-Kurti (right) and postdoctoral researcher Adisu Negeri examine mutant corn plants for hypersensitive response lesions.

Balint-Kurti and colleagues demonstrated MAGIC's usefulness when examining "hypersensitive response" in maize. Hypersensitive response is a defense mechanism used by all plants in which one or a few cells surrounding the site of pathogen attack essentially commit suicide to prevent further spread of the pathogen.

In a study published in *Genetics*, the researchers reported on mutant gene *Rp1-D21*, a partially dominant disease-resistance gene that causes hypersensitive-response lesions to form spontaneously all over the plant—whether the pathogen is present or not. They found that the gene's phenotype is profoundly affected by genetic background. The scientists crossed a plant containing *Rp1-D21* with offspring of B73 and Mo17, two popular maize inbred lines. B73 partially suppresses the *Rp1-D21* phenotype, and Mo17 partially enhances it. With this approach, the scientists identified a genomic location involved in the pathway controlling the start or local spread of hypersensitive response.

"By using the MAGIC technique, breeders can effectively screen the vast amount of genetic diversity present in maize—and in other plant species—for

lines and genomic locations that have genes useful for controlling important plant traits, such as drought tolerance, sugar accumulation, and aluminum tolerance," says Balint-Kurti. "In the present study, we are identifying variation controlling the plant defense response, which has been essentially invisible to us until now. This brings us one step closer to producing disease-tolerant cultivars."

More hypersensitive-response studies are under way. Funded by the National Science Foundation, the scientists are now using MAGIC to screen the 5,000-line Nested Association Mapping population—recently established by ARS scientists—for other genomic regions responsible for hypersensitive response. (See story on page 4 of this issue.)—By **Stephanie Yao, ARS.**

This research is part of Plant Genetic Resources, Genomics, and Genetic Improvement, an ARS national program (#301) described at www.nps.ars.usda.gov.

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